



SEQUENCE LISTING

<110> POLYMERPOULOUS, MIHAEL  
LAVEDAN, CHRISTIAN  
LEROY, ELISABETH  
NUSSBAUM, ROBERT  
JOHNSON, WILLIAM  
DUVOISIN, ROGER

<120> CLONING OF A GENE MUTATION FOR PARKINSON'S DISEASE

<130> 31978-164334

<140> 09/446,628

<141> 1998-06-25

<160> 25

<170> PatentIn Ver. 2.1

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Gly  
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Ser Lys Thr Lys Lys Glu Gly Val Val His Gly Val Thr Thr  
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attgtgctta tatcaaagat gatantaaa gtatctagt attagtgtgg cccagtatca 167

agattcctat gaaattgtaa aacaatcact gagcatctaa gaacatatc 216

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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| Tyr     | Ser | Gly | Leu | Tyr | Leu | Glu | Ser | Glu | Arg | Leu | Tyr | Ser | Ala | Leu | Ala |     |
|         |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Leu     | Tyr | Ser | Gly | Leu | Gly | Leu | Tyr | Val | Ala | Leu | Val | Ala | Leu | Ala | Leu |     |
|         |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ala     | Ala | Leu | Ala | Ala | Leu | Ala | Gly | Leu | Leu | Tyr | Ser | Thr | His | Arg | Leu |     |
|         | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Tyr     | Ser | Gly | Leu | Asn | Gly | Leu | Tyr | Val | Ala | Leu | Ala | Leu | Ala | Gly | Leu |     |
| 65      |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala     | Leu | Ala | Ala | Leu | Ala | Gly | Leu | Tyr | Leu | Tyr | Ser | Thr | His | Arg | Leu |     |
|         |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Tyr     | Ser | Gly | Leu | Gly | Leu | Tyr | Val | Ala | Leu | Leu | Glu | Thr | Tyr | Arg | Val |     |
|         |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Ala     | Leu | Gly | Leu | Tyr | Ser | Glu | Arg | Leu | Tyr | Ser | Thr | His | Arg | Leu | Tyr |     |
|         |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Ser     | Gly | Leu | Gly | Leu | Tyr | Val | Ala | Leu | Val | Ala | Leu | His | Ile | Ser | Gly |     |
|         | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| Leu     | Tyr | Val | Ala | Leu | Ala | Leu | Ala | Thr | His | Arg | Val | Ala | Leu | Ala | Leu |     |
| 145     |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |
| Ala     | Gly | Leu | Leu | Tyr | Ser | Thr | His | Arg | Leu | Tyr | Ser | Gly | Leu | Gly | Leu |     |
|         |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Asn     | Val | Ala | Leu | Thr | His | Arg | Ala | Ser | Asn | Val | Ala | Leu | Gly | Leu | Tyr |     |
|         |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Gly     | Leu | Tyr | Ala | Leu | Ala | Val | Ala | Leu | Val | Ala | Leu | Thr | His | Arg | Gly |     |
|         |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |

Leu Tyr Val Ala Leu Thr His Arg Ala Leu Ala Val Ala Leu Ala Leu  
210 215 220

Ala Gly Leu Asn Leu Tyr Ser Thr His Arg Val Ala Leu Gly Leu Gly  
225 230 235 240

Leu Tyr Ala Leu Ala Gly Leu Tyr Ser Glu Arg Ile Leu Glu Ala Leu  
245 250 255

Ala Ala Leu Ala Ala Leu Ala Thr His Arg Gly Leu Tyr Pro His Glu  
260 265 270

Val Ala Leu Leu Tyr Ser Leu Tyr Ser Ala Ser Pro Gly Leu Asn Leu  
275 280 285

Glu Gly Leu Tyr Leu Tyr Ser Ala Ser Asn Gly Leu Gly Leu Gly Leu  
290 295 300

Tyr Ala Leu Ala Pro Arg Gly Leu Asn Gly Leu Gly Leu Tyr Ile Leu  
305 310 315 320

Glu Leu Glu Gly Leu Ala Ser Pro Met Glu Thr Pro Arg Val Ala Leu  
325 330 335

Ala Ser Pro Pro Arg Ala Ser Pro Ala Ser Asn Gly Leu Ala Leu Ala  
340 345 350

Thr Tyr Arg Gly Leu Met Glu Thr Pro Arg Ser Glu Arg Gly Leu Gly  
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Gly Leu Pro Arg Gly Leu Ala Leu Ala  
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<211> 394

<212> PRT

<213> Rattus norvegicus

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35 40 45

Ala Ala Leu Ala Ala Leu Ala Gly Leu Leu Tyr Ser Thr His Arg Leu  
50 55 60

Tyr Ser Gly Leu Asn Gly Leu Tyr Val Ala Leu Ala Leu Ala Gly Leu  
65 70 75 80

Ala Leu Ala Ala Leu Ala Gly Leu Tyr Leu Tyr Ser Thr His Arg Leu  
                                     85                                    90                                    95

Tyr Ser Gly Leu Gly Leu Tyr Val Ala Leu Leu Glu Thr Tyr Arg Val  
                                     100                                    105                                    110

Ala Leu Gly Leu Tyr Ser Glu Arg Leu Tyr Ser Thr His Arg Leu Tyr  
                                     115                                    120                                    125

Ser Gly Leu Gly Leu Tyr Val Ala Leu Val Ala Leu His Ile Ser Gly  
                                     130                                    135                                    140

Leu Tyr Val Ala Leu Thr His Arg Thr His Arg Val Ala Leu Ala Leu  
 145                                    150                                    155                                    160

Ala Gly Leu Leu Tyr Ser Thr His Arg Leu Tyr Ser Gly Leu Gly Leu  
                                     165                                    170                                    175

Asn Val Ala Leu Thr His Arg Ala Ser Asn Val Ala Leu Gly Leu Tyr  
                                     180                                    185                                    190

Gly Leu Tyr Ala Leu Ala Val Ala Leu Val Ala Leu Thr His Arg Gly  
                                     195                                    200                                    205

Leu Tyr Val Ala Leu Thr His Arg Ala Leu Ala Val Ala Leu Ala Leu  
                                     210                                    215                                    220

Ala Gly Leu Asn Leu Tyr Ser Thr His Arg Val Ala Leu Gly Leu Gly  
 225                                    230                                    235                                    240

Leu Tyr Ala Leu Ala Gly Leu Tyr Ala Ser Asn Ile Leu Glu Ala Leu  
                                     245                                    250                                    255

Ala Ala Leu Ala Ala Leu Ala Thr His Arg Gly Leu Tyr Pro His Glu  
                                     260                                    265                                    270

Val Ala Leu Leu Tyr Ser Leu Tyr Ser Ala Ser Pro Gly Leu Asn Met  
                                     275                                    280                                    285

Glu Thr Gly Leu Tyr Leu Tyr Ser Gly Leu Tyr Gly Leu Gly Leu Gly  
                                     290                                    295                                    300

Leu Tyr Thr Tyr Arg Pro Arg Gly Leu Asn Gly Leu Gly Leu Tyr Ile  
 305                                    310                                    315                                    320

Leu Glu Leu Glu Gly Leu Ala Ser Pro Met Glu Thr Pro Arg Val Ala  
                                     325                                    330                                    335

Leu Ala Ser Pro Pro Arg Ser Glu Arg Ser Glu Arg Gly Leu Ala Leu  
                                     340                                    345                                    350

Ala Thr Tyr Arg Gly Leu Met Glu Thr Pro Arg Ser Glu Arg Gly Leu  
                                     355                                    360                                    365

Gly Leu Gly Leu Tyr Thr Tyr Arg Gly Leu Asn Ala Ser Pro Thr Tyr  
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Leu Tyr Ser Gly Leu Gly Leu Tyr Val Ala Leu Val Ala Leu Ala Leu  
35 40 45  
Ala Ala Leu Ala Ala Leu Ala Gly Leu Leu Tyr Ser Thr His Arg Leu  
50 55 60  
Tyr Ser Gly Leu Asn Gly Leu Tyr Val Ala Leu Thr His Arg Gly Leu  
65 70 75 80  
Ala Leu Ala Ala Leu Ala Gly Leu Leu Tyr Ser Thr His Arg Leu Tyr  
85 90 95  
Ser Gly Leu Gly Leu Tyr Val Ala Leu Leu Glu Thr Tyr Arg Val Ala  
100 105 110  
Leu Gly Leu Tyr Ser Glu Arg Leu Tyr Ser Thr His Arg Leu Tyr Ser  
115 120 125  
Gly Leu Gly Leu Tyr Val Ala Leu Val Ala Leu Gly Leu Asn Gly Leu  
130 135 140  
Tyr Val Ala Leu Ala Leu Ala Ser Glu Arg Val Ala Leu Ala Leu Ala  
145 150 155 160  
Gly Leu Leu Tyr Ser Thr His Arg Leu Tyr Ser Gly Leu Gly Leu Asn  
165 170 175  
Ala Leu Ala Ser Glu Arg His Ile Ser Leu Glu Gly Leu Tyr Gly Leu  
180 185 190  
Tyr Ala Leu Ala Val Ala Leu Pro His Glu Ser Glu Arg Gly Leu Tyr  
195 200 205  
Ala Leu Ala Gly Leu Tyr Ala Ser Asn Ile Leu Glu Ala Leu Ala Ala  
210 215 220  
Leu Ala Ala Leu Ala Thr His Arg Gly Leu Tyr Leu Glu Val Ala Leu  
225 230 235 240  
Leu Tyr Ser Leu Tyr Ser Gly Leu Gly Leu Pro His Glu Pro Arg Thr  
245 250 255

His Arg Ala Ser Pro Leu Glu Leu Tyr Ser Pro Arg Gly Leu Gly Leu  
                   260                                  265                                  270

Val Ala Leu Ala Leu Ala Gly Leu Asn Gly Leu Ala Leu Ala Ala Leu  
                   275                                  280                                  285

Ala Gly Leu Gly Leu Pro Arg Leu Glu Ile Leu Glu Gly Leu Pro Arg  
                   290                                  295                                  300

Leu Glu Met Glu Thr Gly Leu Pro Arg Gly Leu Gly Leu Tyr Gly Leu  
                   305                                  310                                  315                                  320

Ser Glu Arg Thr Tyr Arg Gly Leu Gly Leu Gly Leu Asn Pro Arg Gly  
                                   325                                  330                                  335

Leu Asn Gly Leu Gly Leu Thr Tyr Arg Gly Leu Asn Gly Leu Thr Tyr  
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Arg Gly Leu Pro Arg Gly Leu Ala Leu Ala  
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                                   20                                  25                                  30

Leu Tyr Ser Gly Leu Val Ala Leu Val Ala Leu Ala Leu Ala Ala Leu  
                                   35                                  40                                  45

Ala Ala Leu Ala Gly Leu Leu Tyr Ser Thr His Arg Leu Tyr Ser Gly  
                   50                                  55                                  60

Leu Asn Gly Leu Tyr Val Ala Leu Ala Leu Ala Gly Leu Ala Leu Ala  
           65                                  70                                  75                                  80

Ala Leu Ala Gly Leu Tyr Leu Tyr Ser Thr His Arg Leu Tyr Ser Gly  
                                   85                                  90                                  95

Leu Gly Leu Tyr Val Ala Leu Leu Glu Thr Tyr Arg Val Ala Leu Gly  
                                   100                                  105                                  110

Leu Tyr Ser Glu Arg Ala Arg Gly Thr His Arg Leu Tyr Ser Gly Leu  
                   115                                  120                                  125

Gly Leu Tyr Val Ala Leu Val Ala Leu His Ile Ser Gly Leu Tyr Val  
           130                                  135                                  140

Ala Leu Thr His Arg Thr His Arg Val Ala Leu Ala Leu Ala Gly Leu  
           145                                  150                                  155                                  160

Leu Tyr Ser Thr His Arg Leu Tyr Ser Gly Leu Gly Leu Asn Val Ala  
 165 170 175

Leu Ser Glu Arg Ala Ser Asn Val Ala Leu Gly Leu Tyr Gly Leu Tyr  
 180 185 190

Ala Leu Ala Val Ala Leu Val Ala Leu Thr His Arg Gly Leu Tyr Val  
 195 200 205

Ala Leu Thr His Arg Ala Leu Ala Val Ala Leu Ala Leu Ala Gly Leu  
 210 215 220

Asn Leu Tyr Ser Thr His Arg Val Ala Leu Gly Leu Gly Leu Tyr Ala  
 225 230 235 240

Leu Ala Gly Leu Tyr Ala Ser Asn Ile Leu Glu Ala Leu Ala Ala Leu  
 245 250 255

Ala Ala Leu Ala Thr His Arg Gly Leu Tyr Leu Glu Val Ala Leu Leu  
 260 265 270

Tyr Ser Leu Tyr Ser Ala Ser Pro Gly Leu Asn Leu Glu Ala Leu Ala  
 275 280 285

Leu Tyr Ser Gly Leu Asn Ala Ser Asn Gly Leu Gly Leu Gly Leu Tyr  
 290 295 300

Pro His Glu Leu Glu Gly Leu Asn Gly Leu Gly Leu Tyr Met Glu Thr  
 305 310 315 320

Val Ala Leu Ala Ser Asn Ala Ser Asn Thr His Arg Gly Leu Tyr Ala  
 325 330 335

Leu Ala Ala Leu Ala Val Ala Leu Ala Ser Pro Pro Arg Ala Ser Pro  
 340 345 350

Ala Ser Asn Gly Leu Ala Leu Ala Thr Tyr Arg Gly Leu Met Glu Thr  
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Pro Arg Pro Arg Gly Leu Gly Leu Gly Leu Thr Tyr Arg Gly Leu Asn  
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Ala Ser Pro Thr Tyr Arg Gly Leu Pro Arg Gly Leu Ala Leu Ala  
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<210> 8

<211> 405

<212> PRT

<213> Torpedo californica

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Ser Gly Leu Tyr Pro His Glu Ser Glu Arg Pro His Glu Ala Leu Ala  
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 35 40 45  
 Ala Ala Leu Ala Ala Leu Ala Gly Leu Leu Tyr Ser Thr His Arg Leu  
 50 55 60  
 Tyr Ser Gly Leu Asn Gly Leu Tyr Val Ala Leu Gly Leu Asn Ala Ser  
 65 70 75 80  
 Pro Ala Leu Ala Ala Leu Ala Gly Leu Leu Tyr Ser Thr His Arg Leu  
 85 90 95  
 Tyr Ser Gly Leu Asn Gly Leu Tyr Val Ala Leu Gly Leu Asn Ala Ser  
 100 105 110  
 Pro Ala Leu Ala Ala Leu Ala Gly Leu Leu Tyr Ser Thr His Arg Leu  
 115 120 125  
 Tyr Ser Gly Leu Gly Leu Tyr Val Ala Leu Met Glu Thr Thr Tyr Arg  
 130 135 140  
 Val Ala Leu Gly Leu Tyr Thr His Arg Leu Tyr Ser Thr His Arg Leu  
 145 150 155 160  
 Tyr Ser Gly Leu Gly Leu Tyr Val Ala Leu Val Ala Leu Gly Leu Asn  
 165 170 175  
 Ser Glu Arg Val Ala Leu Ala Ser Asn Thr His Arg Val Ala Leu Thr  
 180 185 190  
 His Arg Gly Leu Leu Tyr Ser Thr His Arg Leu Tyr Ser Gly Leu Gly  
 195 200 205  
 Leu Asn Ala Leu Ala Ala Ser Asn Val Ala Leu Val Ala Leu Gly Leu  
 210 215 220  
 Tyr Gly Leu Tyr Ala Leu Ala Val Ala Leu Val Ala Leu Ala Leu Ala  
 225 230 235 240  
 Gly Leu Tyr Val Ala Leu Ala Ser Asn Thr His Arg Val Ala Leu Ala  
 245 250 255  
 Leu Ala Ser Glu Arg Leu Tyr Ser Thr His Arg Val Ala Leu Gly Leu  
 260 265 270  
 Gly Leu Tyr Val Ala Leu Gly Leu Ala Ser Asn Val Ala Leu Ala Leu  
 275 280 285  
 Ala Ala Leu Ala Ala Leu Ala Ser Glu Arg Gly Leu Tyr Val Ala Leu  
 290 295 300  
 Val Ala Leu Leu Tyr Ser Leu Glu Ala Ser Pro Gly Leu His Ile Ser  
 305 310 315 320  
 Gly Leu Tyr Ala Arg Gly Gly Leu Ile Leu Glu Pro Arg Ala Leu Ala  
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Gly Leu Gly Leu Asn Val Ala Leu Ala Leu Ala Gly Leu Gly Leu Tyr  
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 Leu Tyr Ser Gly Leu Asn Thr His Arg Thr His Arg Gly Leu Asn Gly  
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 Leu Pro Arg Leu Glu Val Ala Leu Gly Leu Ala Leu Ala Thr His Arg  
                   370                  375                  380  
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19

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 ttcaagggac gctaggantn tccgcggccc tggaggttcg cactggggag tggggtgaga 180  
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 cgtgtatcgc cctccccagg ccgccaggat ggacgtgttc atgaagggcc tgtccatggc 360  
 caaggagggc gttgtggcag ccgcggagaa aaccaagcag ggggtcaccg aggcggcgga 420  
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 gggctggggg tccccctaca gtgtggagct ggggcccggg cccggggagg ggggttctgg 540  
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 gggggctcca nctgaaaggc cagggaccan tgcantnata aaancacaca nccctctttt 720  
 tcttatcttt tttaccatta ttaatagtta tctgggtgtg aacactttct gtatgccaag 780  
 tactgggtaa aatgtcataa catccatttc ctcatgtaat gcttccgccc attctacagg 840

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taagggaaac tggggttccc attggtagnt aaatttttagg ttcagaaagg cttgaattga 900
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gacaataaca gcaccccgctt cccagggctg gggaaaaagtg aagtgtagcg gggcaggcag 1000
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aggtgggaga gaaactgcaac ccttcagac agaggtgtgg ggcccagtgc agtgataaga 1140
cggggggttaa catgggggtg caggttgtag gatntgggga cccaaaggag cagtgcaggg 1200
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cnaggggagc ntgaggggta tttttggggg cccgatgcc agcacagagc ctgacacaaa 2100
ggatgaggca taagctggtg antgagtatc caaatggtgg aagtgtggag gntgccaggc 2160
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cgggggaatt tcccccttca cctccatccc acttccaagg cactccaaat aaataactga 2280
attagaaatt atccttgttt tgccaaccca cctagcctt cccactcca acccacccaa 2340
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gatggagcca gaagggggaga gttatgagga cccaccccag gaggaatatc aggagtatga 2520
gccagggcg taggggcccga ggagagcccc caccagcagc acaattctgt cctgtccct 2580
gccccgcccc ccagagccag ggctgtcctt agactcctt tccccaatca cgagatcttc 2640
cttccgctct gaggcaaccc cctcggagcc tgtgttagtg tctgtccatc tgtctgtcct 2700
acccgccccg gtccaacccc ggggcatgga cagggccagg gttgcggtcg cggctgggag 2760
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<210> 12

<211> 223

<212> DNA

<213> Homo sapiens

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<222> (94)

<223> a, t, c, g, other or unknown

<400> 12

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gcagggggtg acggaagcag ctgagaagac caaggagggg gtcagtgtatg tgggattaca 180
tttttttttt aaagaaagaa taaattaatt gtgattaaag ttg 223

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<210> 13

<211> 677

<212> DNA

<213> Homo sapiens

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<223> a, t, c, g, other or unknown

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<223> a, t, c, g, other or unknown

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<222> (34)  
<223> a, t, c, g, other or unknown

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<223> a, t, c, g, other or unknown

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<223> a, t, c, g, other or unknown

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<223> a, t, c, g, other or unknown

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<223> a, t, c, g, other or unknown

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<223> a, t, c, g, other or unknown

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<222> (98)  
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<223> a, t, c, g, other or unknown

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<223> a, t, c, g, other or unknown

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 <223> a, t, c, g, other or unknown

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 <223> a, t, c, g, other or unknown

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 <223> a, t, c, g, other or unknown

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 <222> (253)  
 <223> a, t, c, g, other or unknown

<220>  
 <221> modified\_base  
 <222> (262)  
 <223> a, t, c, g, other or unknown

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 ggggaaaang gttngggggn naaccnaaa aaannccnan gggggggggn antnaanttt 120



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tgggaaccca aagcccnagg aggatttttn gtnaanaacg tnacctcnag tgggnecgagg 180
aagaccaagg aaangcccaa cncggttgan cgaggctgtg gtgaacancg tncaacnctg 240
tgcccnccaa nancgtggag gngggggaga acatcscggt cacctccggg gtggtgcgcm 300
aggaggactt gaggccatct kccccccmac aggagggtgt ggcacccmaa garaaagagg 360
aagtggcaga ggaggcccag agtgggggar actagagggc tacaggccag cgtggatgac 420
ctgaagagcg ctctcttgcc ttggacacca tccccctcta gcacaaggag tgcccgctt 480
gagtgcacatg cggctgcccc cgctcttgcc ctctcttcc tggccaccct tgacctgtcc 540
acctgtgctg ctgcaccaac ctcaactgcc tccctcggcc ccaccaccc tctgggtcctt 600
ctgaccccac ttatgctgct gtgaattttt tttttaaatg attccaaata aaacttgagc 660
ccactccaaa aaaaaaa 677

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<210> 14

<211> 1181

<212> DNA

<213> Homo sapiens

<220>

<221> modified\_base

<222> (130)

<223> a, t, c, g, other or unknown

<220>

<221> modified\_base

<222> (140)

<223> a, t, c, g, other or unknown

<220>

<221> modified\_base

<222> (172)

<223> a, t, c, g, other or unknown

<220>

<221> modified\_base

<222> (193)

<223> a, t, c, g, other or unknown

<220>

<221> modified\_base

<222> (329)..(330)

<223> a, t, c, g, other or unknown

<220>

<221> modified\_base

<222> (902)

<223> a, t, c, g, other or unknown

<220>

<221> modified\_base

<222> (965)

<223> a, t, c, g, other or unknown

<220>

<221> modified\_base

<222> (1015)

<223> a, t, c, g, other or unknown

<220>  
 <221> modified\_base  
 <222> (1159)  
 <223> a, t, c, g, other or unknown

<400> 14  
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 ctgcctgtct cctccagcag ctccccaagg gataggctct gcccttggtg gtcgaccctc 120  
 aggcctcgn tctcccaggn cgactctgac gaggggtagg ggggtggtccc cnggaggacc 180  
 cagaggaaaag gcngggacaa gaagggaggg gaaggggaaa gaggaagagg catcatccct 240  
 agcccaaccg ctcccgatct ccacaagagt gctcgtgacc ctaaaacttaa cgtgaggcgc 300  
 aaaagcgccc caaccttttc ccgccttgnn ccaggcaggc ggctggagtt gatggctcac 360  
 cccgcgcccc ctgccccatc cccatccgag atagggacga ggagcacgct gcagggaaaag 420  
 cagcgagcgc cgggagaggg gcgggcagaa gcgctgacaa atcagcggtg ggggcggaga 480  
 gccgaggaga aggagaagga ggaggactag gaggaggagg acggcgacga ccagaagggg 540  
 cccaagagag ggggcgagcg accgagcgcc gcgacgcgaa gtgagggtgcg tgcggggtca 600  
 gcgcagaccc cggcccggcc cctcctgaga gcgtcctggg cgctccctca cgccttgctc 660  
 tcaagccttc tgcctttcca cctcgtgag cggagaactg ggagtggcca ttcgacgaca 720  
 ggttagcggg tttgcctccc actccccag cctcgcgtcg ccggctcaca gcggcctcct 780  
 ctggggacag tcccccccg gtgcccctcc gcccttcctg tgcgctcctt ttccttcttc 840  
 ttctctatta aatattatct gggaattgtt taaatttttt ttttaaaaaa agagagaggc 900  
 gnggaggagt cggagtgtgt gagaagcaga gggactcagg taagtacctg tggatctaaa 960  
 cggngtctt ttggaaatcc tggagaacgc cggatggaga cgaatggctg tgggnaccgg 1020  
 gagggggtgg tgctgccatg aggaccgctg ggccaggctc ctgggagggt agtacttgct 1080  
 ctttggggag ctaaggaaaag agacttgacc tggctttcgt cctgcttctg atattccctt 1140  
 ctccacaagg gctgagagnt taggctgctt ctccgggatc c 1181

<210> 15  
 <211> 536  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (422)  
 <223> a, t, c, g, other or unknown

<220>  
 <221> modified\_base  
 <222> (481)  
 <223> a, t, c, g, other or unknown

<220>  
 <221> modified\_base  
 <222> (490)  
 <223> a, t, c, g, other or unknown

<220>  
 <221> modified\_base  
 <222> (525)  
 <223> a, t, c, g, other or unknown

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 tttccccgaa agttctcatt caaagtgtat tttatgtttt ccagtgtggt gtaaagaaat 120  
 tcattagcca tggatgtatt catgaaagga ctttcaaagg ccaaggaggg agttgtggct 180  
 gctgctgaga aaaccaaaca ggggtgtggc gaagcagcag gaaagacaaa agagggtgtt 240

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ctctatgtag gtaggtaaac cccaaatgtc agtttggtgc ttgttcatga gtgatgggtt 300
aggataacaa tactctaaat gctggtagtt ctctctcttg attcattttt gcacatttgc 360
ttgtcaaaaa ggtggactga gtcagaggta tgtgtaggta ggtgaatgtg aacgtgtgta 420
tntgagctaa tagtaaaaaat gcgactgttt gcttttcaga tttttaattt tgcctaatat 480
ntatgacttn ttaaaatgaa tgtttctgta ctacataatt ctatntcaga gacagt 536

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<210> 16

<211> 650

<212> DNA

<213> Homo sapiens

<220>

<221> modified\_base

<222> (214)

<223> a, t, c, g, other or unknown

<220>

<221> modified\_base

<222> (476)

<223> a, t, c, g, other or unknown

<400> 16

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caaaattatc ttctcactgg gccccgggtg tatctcattc ttttttctcc tctgtaagtt 120
gacatgtgat gtgggaacaa aggggataaa gtcattattt tgtgctaaaa tcgtaattgg 180
agaggacctc ctgttagctg ggctttcttc tatntattgt ggtggttagg agttccttct 240
tctagtttta ggatataat atataatttt tctttccctg aagatataat aatataatata 300
cttctgaaga ttgagatttt taaattagtt gtattgaaaa ctagctaata agcaatttaa 360
ggctagcttg agacttatgt cttgaatttg tttttgtagg ctccaaaacc aaggagggag 420
tggtgcatgg tgtggcaaca ggtaagctcc attgtgctta tatcaaagat gatantaaa 480
gtatctagtg attagtgtgg ccagtatca agattcctat tgaaattgta aaacaatcac 540
tgagcatcta agaacatata agtcttattg aaactgaatt ctttataaag tattttttaa 600
taggtaaata ttgattataa ataaaaaata tacttgccaa gaataatgag 650

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<210> 17

<211> 504

<212> DNA

<213> Homo sapiens

<220>

<221> modified\_base

<222> (117)

<223> a, t, c, g, other or unknown

<400> 17

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atatcttagc caagattcaa tgtttggttg aaccacactc acttgacatc ttggtggctt 60
ttgtttcttc tgaccactca gttatctatg gcatgtgtag atacagggtg atggaancga 120
tggttagtgg aagtggaaatg attttaagtc actgttattc taccaccctt taatctgttg 180
ttgtctttta tttgtaccag tggctgagaa gaccaaaagag caagtgacaa atgttgagg 240
agcagtgggtg acgggtgtga cagcagtagc ccagaagaca gtggagggag caggagagcat 300
tgcagcagcc actggctttg tcaaaaagga ccagttgggc aaggtatggc tgtgtacgtt 360
ttgtgttaca tttataagct ggtgagatta cgtttcattt tcatgtgaag cctggaggca 420
ggagcaagat acttactgtg gggaacggct acctgaccct ccccttgtga aaaagtgtca 480
cctttatatt ggtcttgctt gttt 504

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<210> 18  
 <211> 726  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (553)  
 <223> a, t, c, g, other or unknown

<400> 18  
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 tgtggagttt agaatgccag tagtaatat aagggtgtgcc attttcaaga tccgtggcca 120  
 acatccctat atgtaagatt ttccaaaac atggttctga tttttaaaag tgaaaaatgc 180  
 tacttcatca tgttcttttt gtgcttctta ctttaaatat tagaatgaag aaggagcccc 240  
 acaggaagga attctggaag atatgcctgt ggatcctgac aatgaggctt atgaaatgcc 300  
 ttctgaggta ggagtccaag ctgaatcttt ctaacaagac agtaccaaaa acctgtcatt 360  
 gtcacatttc tctttcatta gtgcttagtg agaatcattt gctctctaca tgctcattag 420  
 tggacaactt gcaagttaag aatagttttt acatttttaa agggtcctta aaaaaaaaga 480  
 ggaggaggaa gatgaagaag aggaagaaag gatgtaaaag aaatcatatg tagtccacat 540  
 agcttaatat acntactact tgaccttcta caggaaaagc tttactaacc cctgcattag 600  
 agaatatatt tttttgcaaa aacattgatt gtaaatttta gtgtaaagtg gggagccatt 660  
 tctatctca ttggctgtcc agtgcctgat cgtaattgaa acttatacta acagtgtgtg 720  
 ctgtct 726

<210> 19  
 <211> 1596  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (415)  
 <223> a, t, c, g, other or unknown

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 <221> modified\_base  
 <222> (486)  
 <223> a, t, c, g, other or unknown

<220>  
 <221> modified\_base  
 <222> (585)  
 <223> a, t, c, g, other or unknown

<220>  
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 <222> (1119)  
 <223> a, t, c, g, other or unknown

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 <222> (1419)  
 <223> a, t, c, g, other or unknown

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<222> (1503)  
 <223> a, t, c, g, other or unknown

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 <222> (1549)  
 <223> a, t, c, g, other or unknown

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 <222> (1554)  
 <223> a, t, c, g, other or unknown

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 <222> (1561)  
 <223> a, t, c, g, other or unknown

<220>  
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 <222> (1581)  
 <223> a, t, c, g, other or unknown

<220>  
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 <222> (1589)  
 <223> a, t, c, g, other or unknown

<400> 19  
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 ttccaatgtg cccagtcattg acatttctca aagtttttac agtgtatctc gaagtcttcc 180  
 atcagcagtg attgaagcat ctgtacctgc cccactcag catttcggtg cttcccttcc 240  
 actgaagtga atacatggta gcagggtctt tgtgtgctgt ggattttgtg gcttcaatct 300  
 acgatgttaa aacaaattaa aaacacctaa gtgactacca cttatttcta aatcctcact 360  
 attttttgtg tgctgttgtt cagaagttgt tagtgatttg ctatcatata ttatnagatt 420  
 tttagggtgc ttttaattgat actgtctaag aataatgacg tattgtgaaa ttgtttaata 480  
 tataatnatac ttaaaaaatat gtgagcatga aactatgcac ctataatact aaatatgaaa 540  
 ttttaccatt ttgcgatgtg ttttattcac ttgtgtttgt atatnaatgg tgagaattaa 600  
 aataaaacgt tatctcattg caaaaatatt ttatttttat cccatctcac ttttaataata 660  
 aaaatcatgc ttataagcaa catgaattaa gaactgacac aaaggacaaa aatataaagt 720  
 tattaatagc catttgaaga aggaggaatt ttagaagagg tagagaaaat ggaacattaa 780  
 ccctacactc ggaattccct gaagcaacac tgccagaagt gtgttttggg atgcactggg 840  
 tccttaagtg gctgtgatta attattgaaa gtgggtgtgt gaagacccca actactattg 900  
 tagagtgggc tatttctccc ttcaatcctg tcaatgtttg ctttacgtat tttggggaac 960  
 tgttgtttga tgtgtatgtg tttataattg ttatacattt ttaattgagc cttttattaa 1020  
 catatattgt tatttttgtc tcgaaataat tttttagtta aaatctattt tgtctgatat 1080  
 tgggtgtgaat gctgtacctt tctgacaata aataatatnc gaccatgaat aaaaaaaaaa 1140  
 aaaaagtggg ttcccgggaa ctaagcagtg tagaagatga ttttgactac accctcctta 1200  
 gagagccata agacacatta gcacatatta gcacattcaa ggctctgaga gaatgtgggt 1260  
 aactttgttt aactcagcat tctcactttt ttttttttaa tcatcagaaa ttctctctct 1320  
 ctctctcttt ttctctctgt ctcttttttt tttttttttt ttttacagga aatgccttta 1380  
 aacatcggtt ggaactacca gagtcacctt aaaggaggna tcaattctct aggactggat 1440  
 aaaaatttca tgggcctcct ttaaaatgtt gcccataat atggaattct aggggttttt 1500  
 centaggggg aagggttttt tctcttttctn ggggaggatc cttttaacnc cccngggggg 1560  
 ngccccgaaa ataaacttgg ngggggggna aaactt 1596

<210> 20  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 20  
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20

<210> 21  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 21  
 ccttggtctt ctcagctgt

20

<210> 22  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 22  
 agcgtggatg acctgaagag

20

<210> 23  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 23  
 agcacaggtg gacaggccaa g

21

<210> 24  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 24  
 gatatgttct tagatgctca g

21

<210> 25  
<211> 14  
<212> PRT  
<213> Homo sapiens

<400> 25  
Gly Ser Lys Thr Lys Glu Gly Val Val His Gly Val Thr Thr  
1 5 10